WHAT IS CLAIMED IS:

1. A method of detecting a prostate cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

2. The method of claim 1, wherein the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.

3. The method of claim 1, wherein the biological sample is a tissue sample.

4. The method of claim 1, wherein the biological sample comprises isolated nucleic acids.

5. The method of claim 4, wherein the nucleic acids are mRNA.

6. The method of claim 4, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

7. The method of claim 1, wherein the polynucleotide comprises a sequence as shown in Tables 1-16.

8. The method of claim 1, wherein the polynucleotide is labeled.

9. The method of claim 8, wherein the label is a fluorescent label.

10. The method of claim 1, wherein the polynucleotide is immobilized on a solid surface.

11. The method of claim 1, wherein the patient is undergoing a therapeutic regimen to treat prostate cancer.

12. The method of claim 1, wherein the patient is suspected of having prostate cancer.

13. A method of monitoring the efficacy of a therapeutic treatment of prostate cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a prostate cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring the efficacy of the therapy.

14. The method of claim 13, further comprising the step of: (iii) comparing the level of the prostate cancer-associated transcript to a level of the prostate cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

15. The method of claim 13, wherein the patient is a human.

16. A method of monitoring the efficacy of a therapeutic treatment of prostate cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a prostate cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16, wherein the polypeptide specifically binds to the prostate cancer-associated antibody, thereby monitoring the efficacy of the therapy.

17. The method of claim 16, further comprising the step of: (iii) comparing the level of the prostate cancer-associated antibody to a level of the prostate cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

18. The method of claim 16, wherein the patient is a human.

19. A method of monitoring the efficacy of a therapeutic treatment of prostate cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a prostate cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring the efficacy of the therapy.

20. The method of claim 19, further comprising the step of: (iii) comparing the level of the prostate cancer-associated polypeptide to a level of the prostate cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

21. The method of claim 19, wherein the patient is a human.

22. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-16.

23. The nucleic acid molecule of claim 22, which is labeled.

24. The nucleic acid of claim 23, wherein the label is a fluorescent label

25. An expression vector comprising the nucleic acid of claim 22.

26. A host cell comprising the expression vector of claim 25.

27. An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-16.

28. An antibody that specifically binds a polypeptide of claim 27.

29. The antibody of claim 28, further conjugated to an effector component.

30. The antibody of claim 29, wherein the effector component is a fluorescent label.

31. The antibody of claim 29, wherein the effector component is a radioisotope or a cytotoxic chemical.

32. The antibody of claim 29, which is an antibody fragment.

33. The antibody of claim 29, which is a humanized antibody

34. A method of detecting a prostate cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody of claim 28.

35. The method of claim 34, wherein the antibody is further conjugated to an effector component.

36. The method of claim 35, wherein the effector component is a fluorescent label.

37. A method of detecting antibodies specific to prostate cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-16.

38. A method for identifying a compound that modulates a prostate cancer-associated polypeptide, the method comprising the steps of:

(i) contacting the compound with a prostate cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16; and

(ii) determining the functional effect of the compound upon the polypeptide.

39. The method of claim 38, wherein the functional effect is a physical effect.

40. The method of claim 38, wherein the functional effect is a chemical effect.

41. The method of claim 38, wherein the polypeptide is expressed in a eukaryotic host cell or cell membrane.

42. The method of claim 38, wherein the functional effect is determined by measuring ligand binding to the polypeptide.

43. The method of claim 38, wherein the polypeptide is recombinant.

44. A method of inhibiting proliferation of a prostate cancer-associated cell to treat prostate cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified using the method of claim 38.

45. The method of claim 44, wherein the compound is an antibody.

46. The method of claim 45, wherein the patient is a human.

47. A drug screening assay comprising the steps of

(i) administering a test compound to a mammal having prostate cancer or a cell isolated therefrom;

(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of prostate cancer.

48. The assay of claim 47, wherein the control is a mammal with prostate cancer or a cell therefrom that has not been treated with the test compound.

49. The assay of claim 47, wherein the control is a normal cell or mammal.

50. A method for treating a mammal having prostate cancer comprising administering a compound identified by the assay of claim 47.

51. A pharmaceutical composition for treating a mammal having prostate cancer, the composition comprising a compound identified by the assay of claim 47 and a physiologically acceptable excipient.

52. The method according to claim 1,wherein said biological sample is contacted with a plurality of polynucleotides comprising a first polynucleotide that selectively hybridizes to a sequence at least 80% identical to a first sequence as shown in Tables 1-16; and a second polynucleotide that selectively hybridizes to a second sequence at least 80% identical to a second sequence as shown in Tables 1-16.

53. A method according to claim 52, wherein the plurality of polynucleotides comprises a third polynucleotide that selectively hybridizes to a sequence at least 80% identical to a third sequence as shown in Tables 1-16..

54. A method of detecting a prostate cancer associated transcript, the method comprising contacting a biological sample from the patient with a plurality of polynucleotides wherein at least two of said polynucleotides selectively hybridize to a difference sequence at least 80% identical to a sequence as shown in Tables 1-16.

55. A method of detecting a prostate cancer, the method comprising the steps of:

(i) providing a biological sample from a patient;

(ii) contacting the biological sample with a first polynucleotide that selectively hybridizes to a sequence at least 80% identical to a first sequence as shown in Tables 1-16 to determine the level of a prostate cancer-associated transcript in the biological sample; and with a second polynucleotide that selectively hybridizes to a second sequence at least 80% identical to a sequence not shown in Tables 1-16; wherein the expression of said second sequence is not substantially changed in prostate cancer, to detemine the level of expression of a control transcript in the biological sample;

(iii) comparing the level of the prostate cancer-associated transcript to a level of the normal tissue associated transcript in the biological sample.

56. A method of quantitating a prostate cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

57. The method of claim 56, wherein the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.

58. The method of claim 56, wherein the biological sample is a tissue sample.

59. The method of claim 56, wherein the biological sample comprises isolated nucleic acids.

60. The method of claim 56, wherein the nucleic acids are mRNA.

61. The method of claim 59, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

62. The method of claim 56, wherein the polynucleotide comprises a sequence as shown in Tables 1-16.

63. The method of claim 56, wherein the polynucleotide is labeled.

64. The method of claim 63, wherein the label is a fluorescent label.

65. The method of claim 56, wherein the polynucleotide is immobilized on a solid surface.

66. The method of claim 56, wherein the patient is undergoing a therapeutic regimen to treat metastatic prostate cancer.

67. The method of claim 56, wherein the patient is suspected of having metastatic prostate cancer.

68. A biochip comprising a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

69. A method of screening drug candidates comprising:

i) providing a cell that expresses an expression profile gene selected from the group consisting of an expression profile gene set forth in Tables 1-16 or fragment thereof;

ii) adding a drug candidate to said cell; and

iii) determining the effect of said drug candidate on the expression of said expression profile gene.

70. A method according to claim 59 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate.